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FIGURE 1.

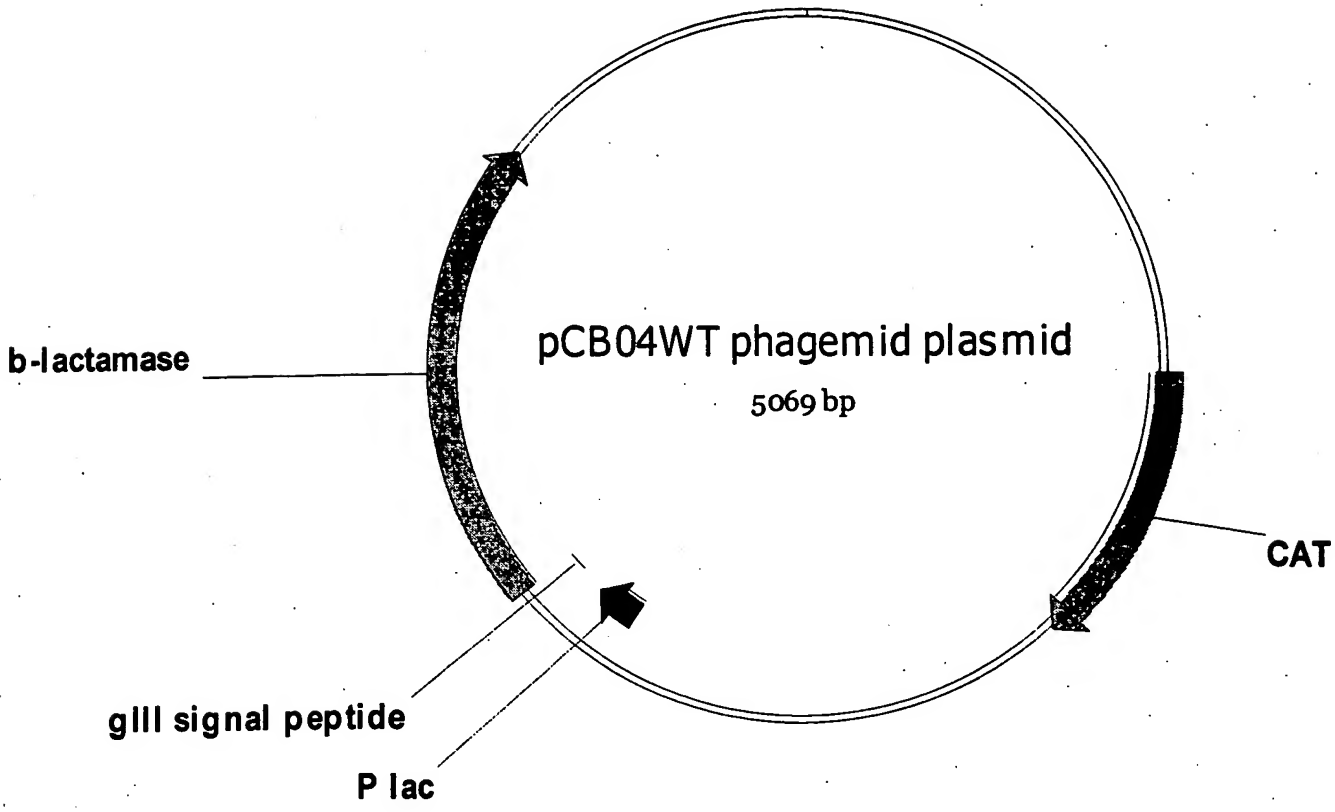

FIGURE 2

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FIGURE 3.

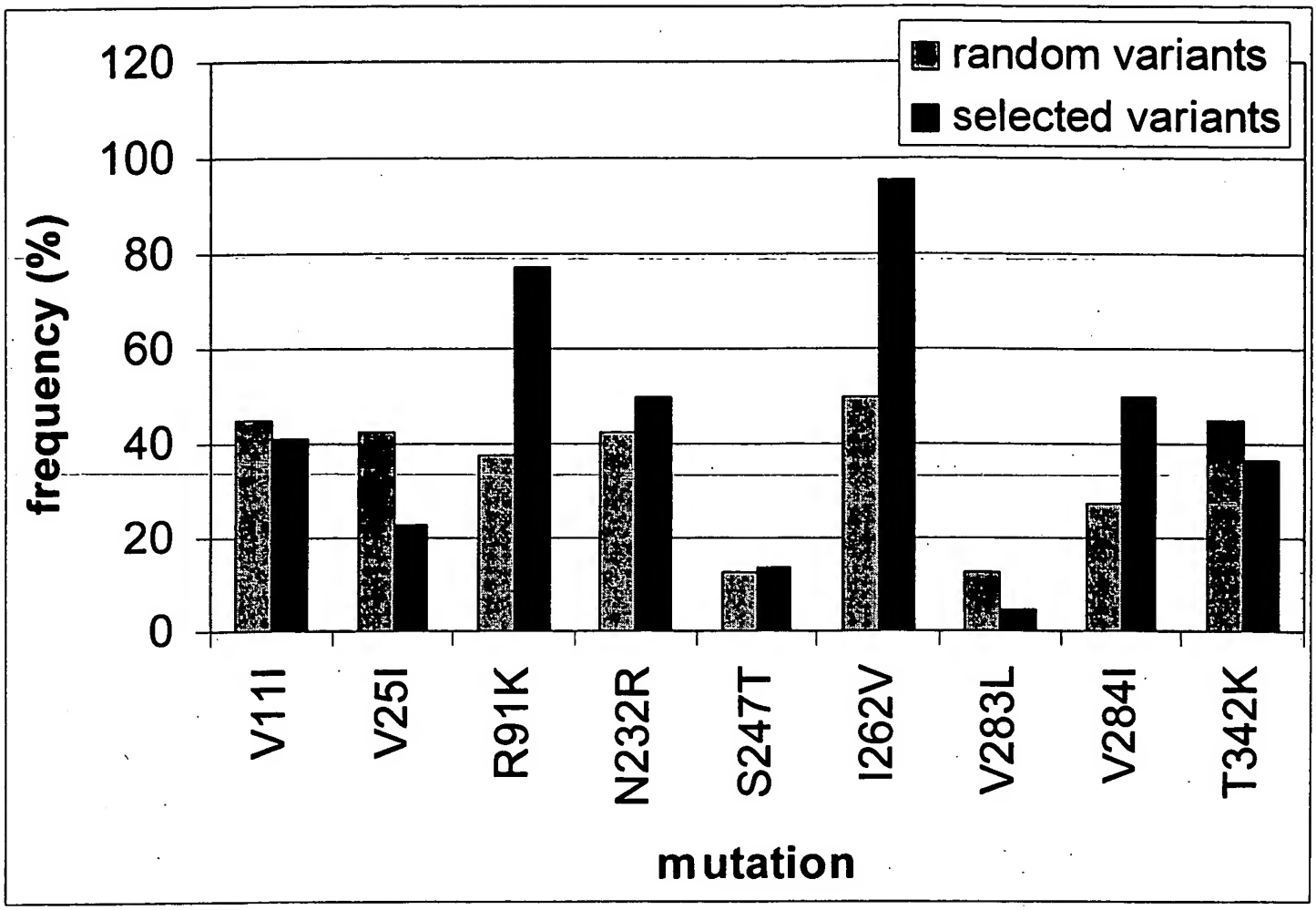

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FIGURE 4.

aa change	parameter	# occur.	rank	
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A13D	0.036	24	15	
V25I	0.194	2	9	
Y41F	-0.232	7	24	
F43Y	-0.092	5	18	
I65V	-0.219	20	22	
R91K	0.367	2	6	
Q95E	0.756	9	1	
R105T	-0.223	2	23	
M106L	-0.175	3	20	
S130A	-0.102	14	19	
A153S	0.669	10	2	
Y170F	-0.256	4	25	
A194S	0.141	4	12	
A208P	-0.021	8	16	
Q219E	-0.446	8	28	
T225S	0.172	3	11	
N226T	-0.198	8	21	
V227A	-0.311	6	27	
N232R	0.442	6	3	
S247T	0.177	4	10	
I262V	0.294	15	8	
V283L	0.334	3	7	
V284I	0.378	19	4	
P295A	-0.299	5	26	
I334L	-0.062	6	17	
T342K	0.107	6	13	
const. C	0.471			

FIGURE 5.

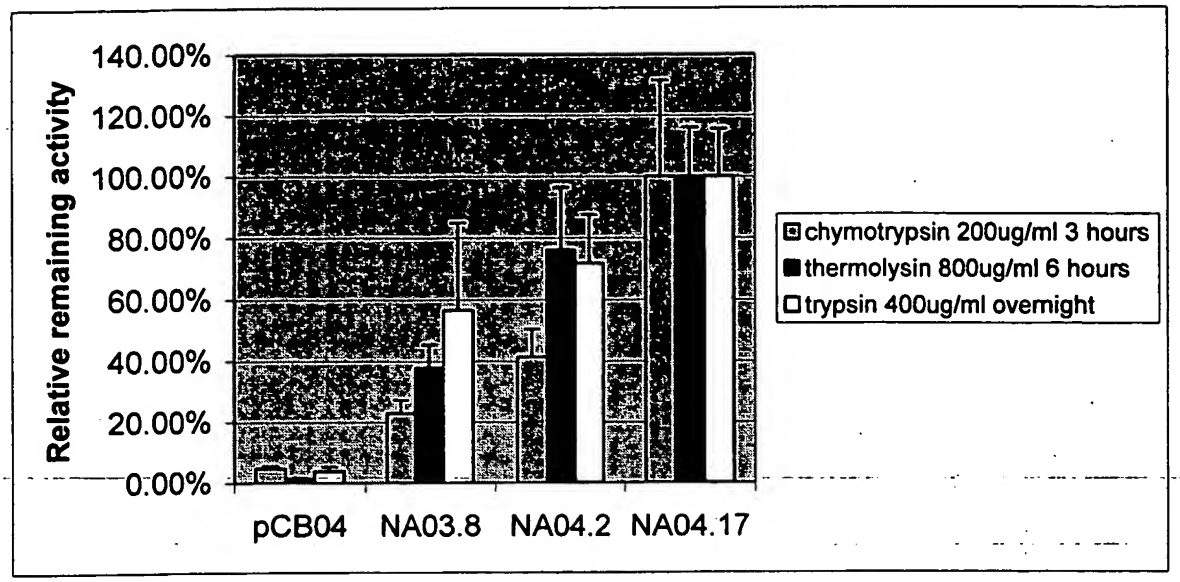

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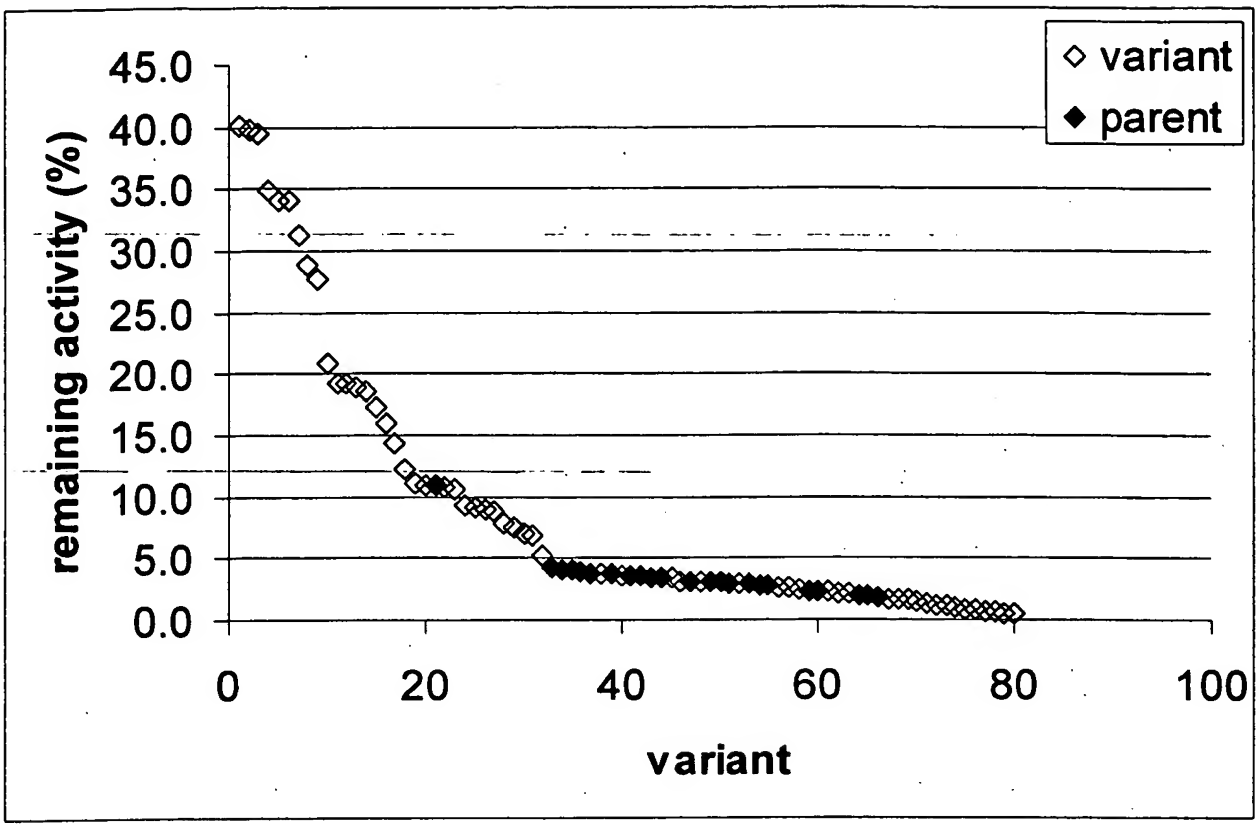
FIGURE 6.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remaining activity (%)
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40.0
35.0
30.0
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0.0
0
20
40
60
80
100
variant

FIGURE 7.

heavy chain:
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vss (SEQ ID NO:2)

linker:
Ggggsggggsggggs (SEQ ID NO:3)

light chain:
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ID NO:4)

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FIGURE 8.

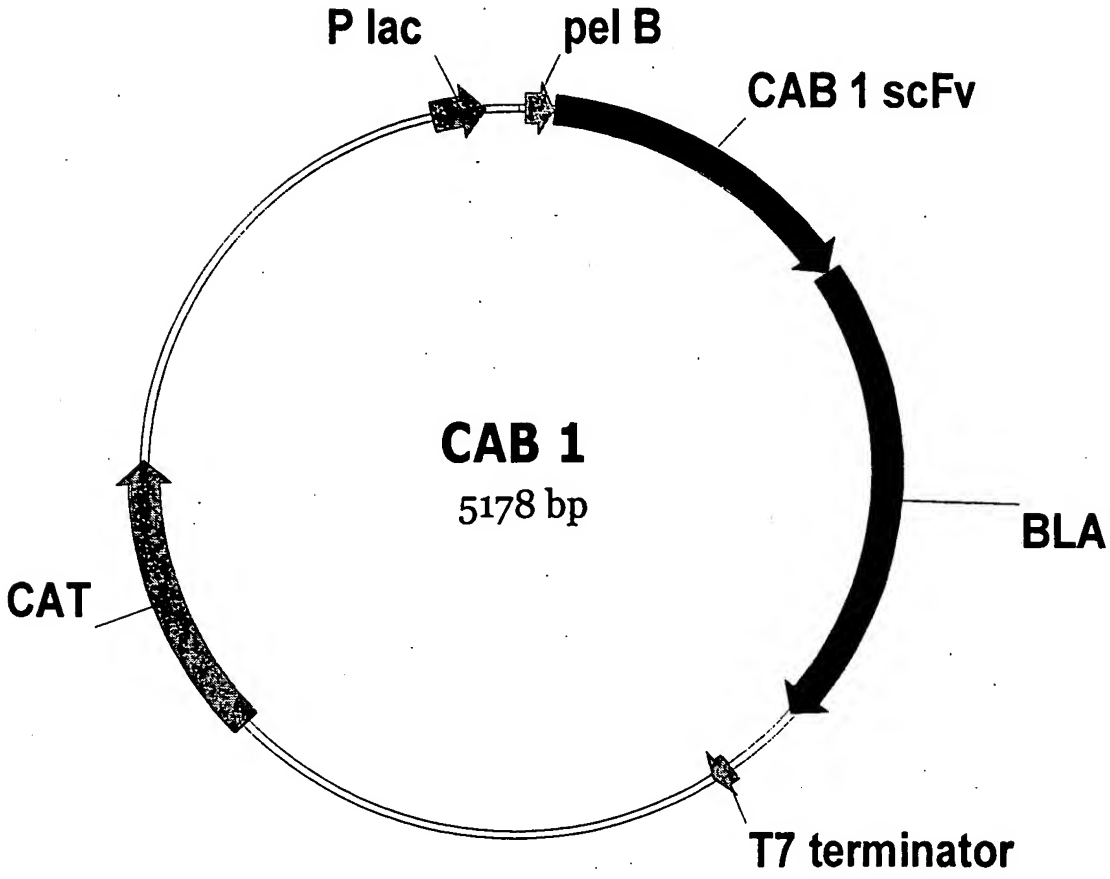

FIGURE 9.

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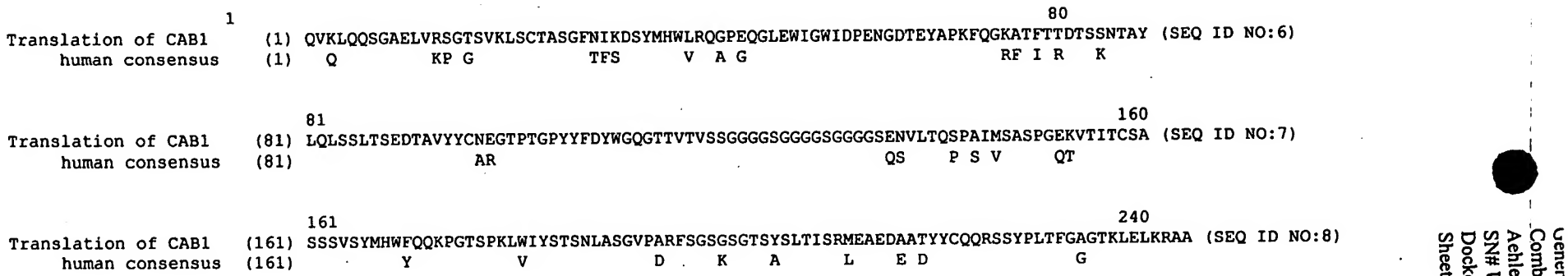
FIGURE 10.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human consensus (1) Q KP G TFS V A G RF I R K
81
160
Translation of CAB1 (81) LQLSSLTSEDTAVYYCNEGTPTGPYYFDYWGQGTTVTVSSGGGGSGGGGSGGGGSENVLTQSPAIMSASPGEKVTITCSA (SEQ ID NO:7)
human consensus (81) AR QS P S V QT
161
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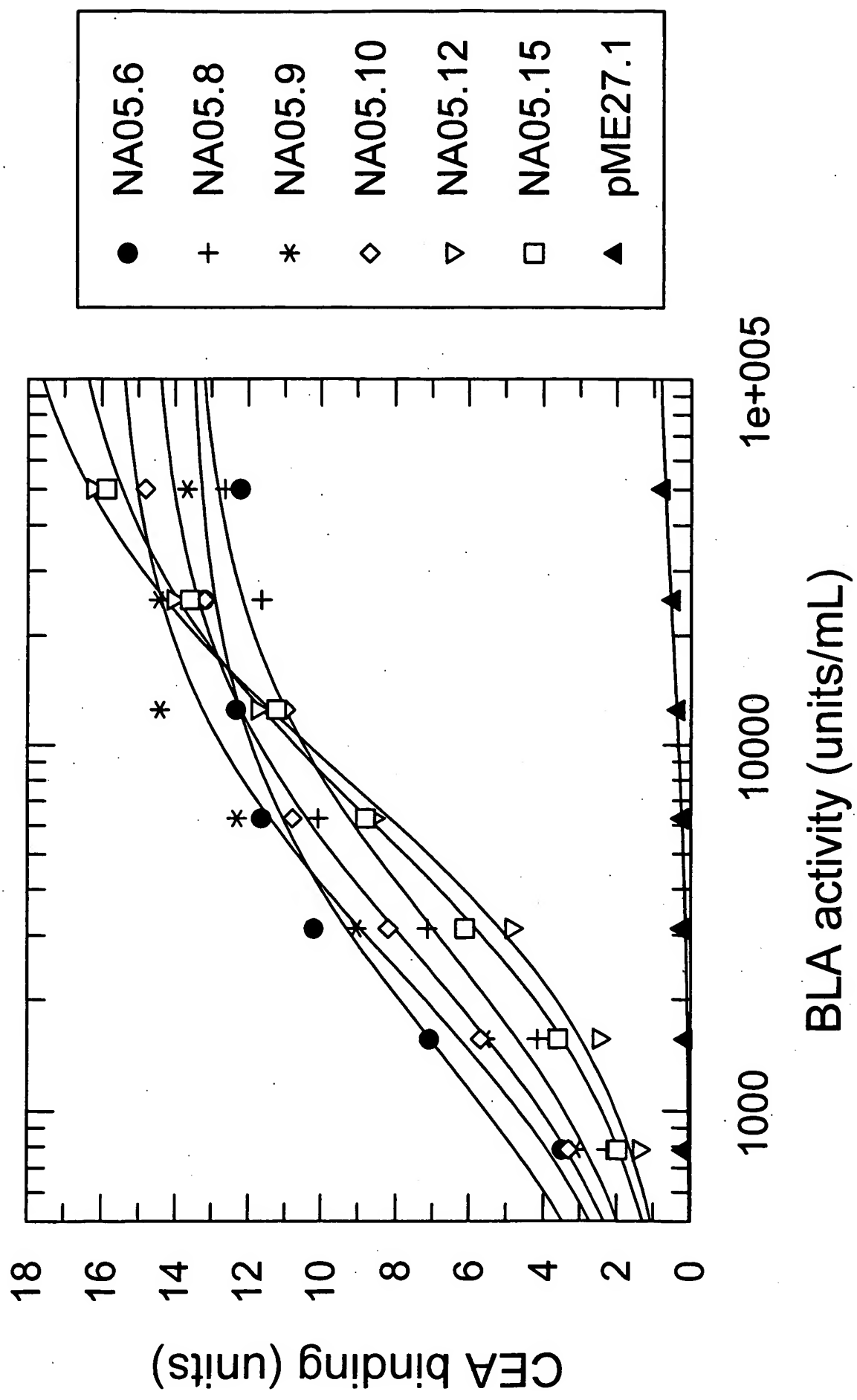
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NA05.8
NA05.9
NA05.10
NA05.12
NA05.15
pME27.1
CEA binding (units)
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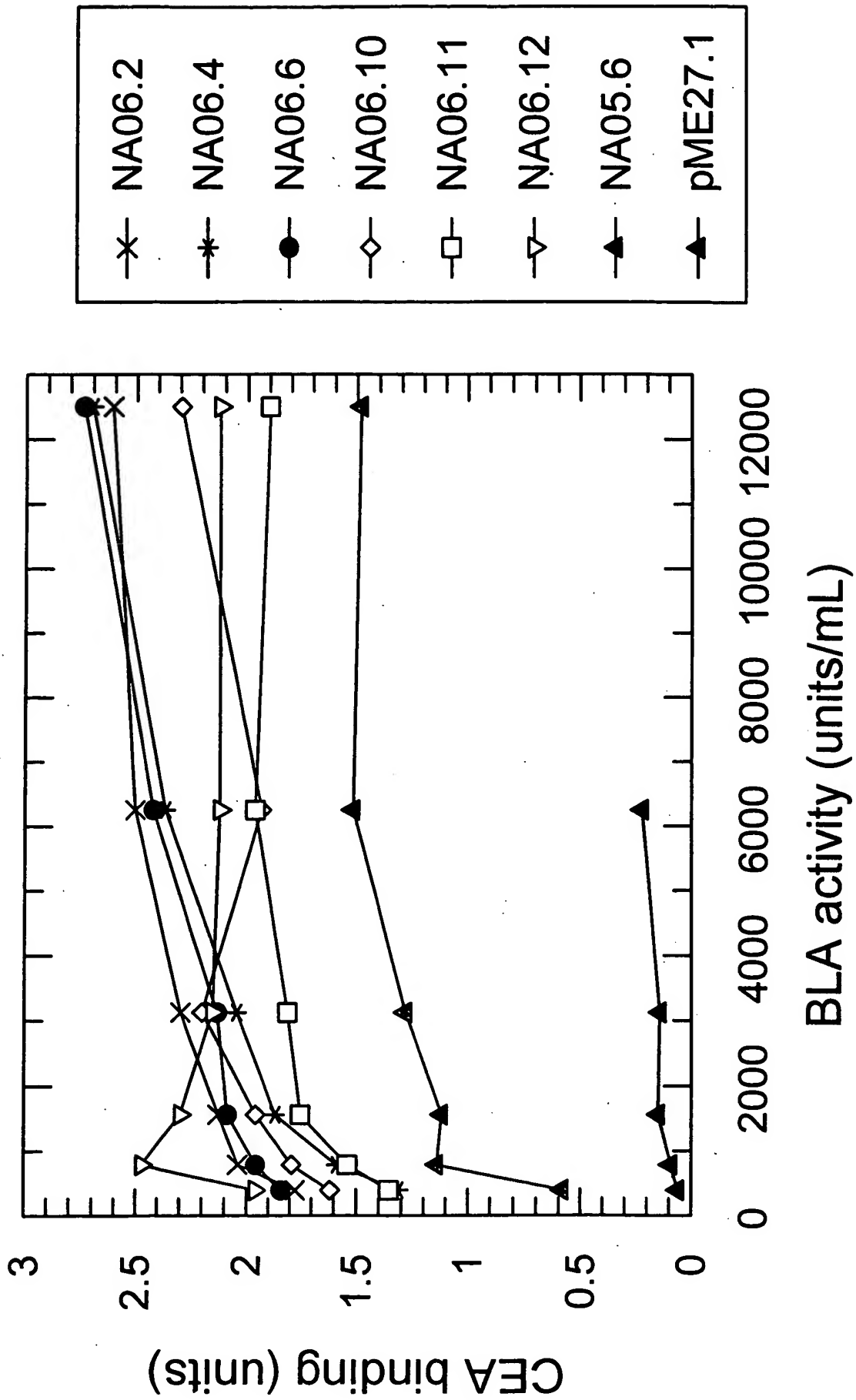
4
6
8
10
12
14
16
18
1000
10000
1e+005
BLA activity (units/mL)

FIGURE 11.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NA06.4
NA06.6
NA06.10
NA06.11
NA06.12
NA05.6
pME27.1
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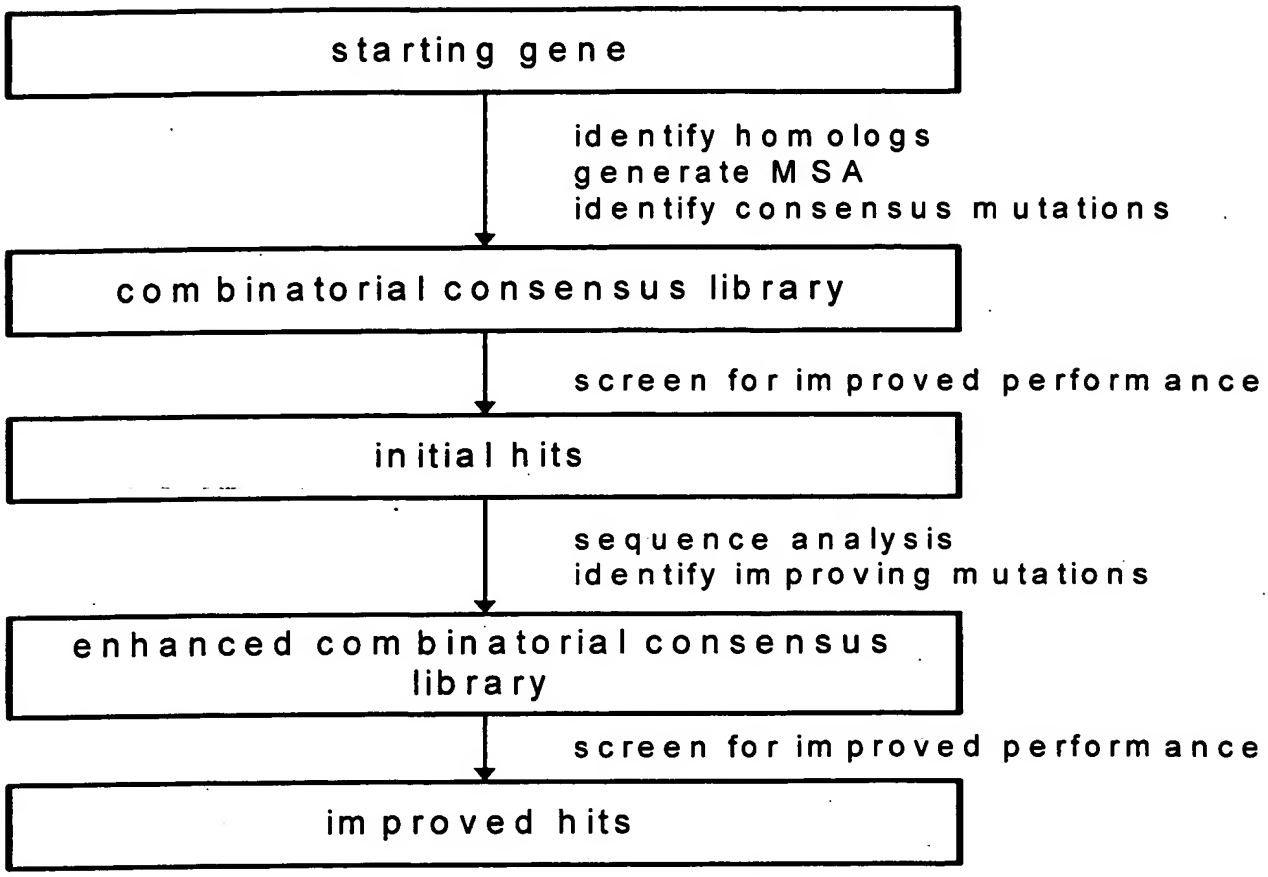
0.5
1
1.5
2
2.5
3
BLA activity (units/mL)
0
2000
4000
6000
8000
10000
12000

FIGURE 12.

FIGURE 13.


starting gene
identify homologs
generate MSA
identify consensus mutations
combinatorial consensus library
screen for improved performance
initial hits
sequence analysis
identify improving mutations
enhanced combinatorial consensus library
screen for improved performance
improved hits